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* * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *
=> file caba caplus embase japio lifesci medline scisearch uspatfull
=> e chou george chin/au
E1            2     CHOU GENICHI/AU
E2           11     CHOU GEORGE/AU
E3            0 --> CHOU GEORGE CHIN/AU
E4            7     CHOU GEORGE CHIN SHENG/AU
E5            1     CHOU GEORGE I N/AU
E6            1     CHOU GEORGE J S/AU
E7            2     CHOU GEORGE JYH SHANN/AU
E8            1     CHOU GEORGE T/AU
E9            5     CHOU GER CHIH/AU
E10           7     CHOU GERCHIH/AU
E11           1     CHOU GI/AU
E12           1     CHOU GIAXUNG/AU
=> s e2-e4 and (dna or nucleic)
   7 FILES SEARCHED...
L1            7 ("CHOU GEORGE"/AU OR "CHOU GEORGE CHIN"/AU OR "CHOU GEORGE CHIN
                SHENG"/AU) AND (DNA OR NUCLEIC)
=> dup rem l1
PROCESSING COMPLETED FOR L1
L2             4 DUP REM L1 (3 DUPLICATES REMOVED)
=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 4 ANSWERS - CONTINUE? Y/(N):y
L2   ANSWER 1 OF 4  CAPLUS  COPYRIGHT 2005 ACS on STN  DUPLICATE 1
AN   2005:98840  CAPLUS
TI   Systemic delivery of non-viral vector expressing SARS viral genomic
     vaccine
IN     ***Chou, George Chin-sheng***
PA   Taiwan
SO   U.S. Pat. Appl. Publ., 21 pp.
     CODEN: USXXCO
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.          KIND   DATE        APPLICATION NO.         DATE
     ---------------     ----   --------    --------------------    --------
PI   US 2005025788        A1    20050203    US 2004-860119          20040604
PRAI US 2003-476244P      P     20030606
AB   The present invention relates to a non-viral vector for SARS Viral Genomic
     Vaccine.  The present invention also relates to a non-targeted lipoplex or
     PEGylated lipoplex formulation for accumulating SARS spike genome in the
     lung to that results in expression of SARS spike protein.  The present
     invention further provides a method of eliciting immunity against SARS
     infection, comprising:   ***DNA***   vaccination using SARS spike protein
     in operative assocn. with a non-viral vector and subsequent local and/or
     systemic immunity against SARS spike protein.  In the present method, the
     subsequent local and/or systemic immunity is primarily by s.c.
     administration and then followed by intra-venously boostering two weeks
     later.

L2   ANSWER 2 OF 4  CAPLUS  COPYRIGHT 2005 ACS on STN  DUPLICATE 2
AN   2005:16961  CAPLUS
DN   142:108387
TI   Appratus, PCR primers and hybridization probe for detecting SARS
     coronavirus (SARS-CV)   ***DNA***
IN     ***Chou, George Chin-Sheng***
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PA Asiagen Corporation, Taiwan
SO U.S. Pat. Appl. Publ., 13 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2005003340	A1	20050106	US 2003-609604	20030701
PRAI	US 2003-609604		20030701		

AB The present invention relates to an assay system and methods for detecting SARS coronavirus (SARS-CV) from the samples (esp. for urine) of suspected patient in the control of SARS to provide updated information of prognosis as well as the criteria for discharging a recovered patient from a hospital. The present invention provides a method for detecting SARS coronavirus (SARS-CV) ***DNA*** , obtained by the PCR amplification, from the samples. The method includes: (a) hybridizing the SARS-CV cDNA with SARS-CV-specific probes wherein the probe linked to magnetic bead; (b) transferring hybridization tubes to magnetic wells for washing; (c) adding blocking soln. into the tubes; (d) adding avidin enzyme complex or streptavidin enzyme complex into the tubes; (e) performing washing reaction to remove interfering material by the aid of magnetic field; (f) suspending magnetic beads; and (g) detecting the luminescent or color change after adding substrate of enzyme. The present invention also relates to an app. for performing the dissocn. of ***nucleic*** acid double strands, hybridization, washing, the sepn. of magnetic beads and thermal control in the same app. The use of this app. largely reduces the time of hybridization (less than 20 min) and the whole process of SARS-CV detection is less than 5 h.

L2 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2005 ACS on STN DUPLICATE 3
AN 2004:934226 CAPLUS
DN 141:395432
TI Preparation of angelicin derivatives linked to acridinium-9-carboxamide derivative or biotin as ***DNA*** labeling reagents and process of preparing ***DNA*** labeling compounds
IN ***Chou, George Chin-Sheng*** ; Wu, Yu-Cheng; Hsu, Po-Ya
PA AsiaGen Corporation, Taiwan
SO U.S. Pat. Appl. Publ., 9 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004219538	A1	20041104	US 2003-428137	20030502
	US 2004219564	A1	20041104	US 2003-689586	20031022
	US 6858742	B2	20050222		
PRAI	US 2003-428137	A3	20030502		

OS MARPAT 141:395432
AB The present invention relates to ***DNA*** labeling reagents comprising a furocoumarin deriv. and a detectable group with or without bound via a binding enhancer, and acridinium-9-carboxamide derivs. for use as chemiluminescent labels. The ***DNA*** labeling reagents are represented by formula Fu-BE-D [wherein Fu represents a furocoumarin deriv. selected from the group consisting of angelicin derivs. and psoralen derivs.; wherein BE represents none or a binding enhancer

selected from the group consisting of C4-12 alkyl, alkenyl, polyalkylamine and polyethylene glycol; and wherein D represents a detectable group selected from the group consisting of biotin, fluorescence, acridinium ester, and acridinium 9-carboxamide]. The present invention also relates to a process of prepg. ***DNA*** labeling compd. Thus, 6-(biotinylamino)hexanoic acid N-succinimide ester was condensed with angelicin deriv. (I) (R = H) in DMSO at room temp. for 36 h to give biotin-linked angelicin deriv. I (R = Q). In another expt., acridine-9-carbonyl chloride was amidated with I (R = H) in CHCl3 at room temp. for 30 min to give I (R = Q1) which was methylated by Me fluorosulfate in CHCl3 for 30 h to give acridinium-9-carboxamide-linked angelicin I (R = Q2).

L2 ANSWER 4 OF 4 USPATFULL on STN
AN 2004:280264 USPATFULL
TI ***DNA*** labeling reagents, acridinium-9-carboxamide derivatives and process of preparing ***DNA*** labeling compounds
IN ***Chou, George Chin-Sheng*** , Hsin-Shi, TAIWAN, PROVINCE OF CHINA
Wu, Yu-Cheng, Hsin-Shi, TAIWAN, PROVINCE OF CHINA
Hsu, Po-Ya, Hsin-Shi, TAIWAN, PROVINCE OF CHINA
PA AsiaGEN Corporation, Tainan Hsien, TAIWAN, PROVINCE OF CHINA (non-U.S. corporation)
PI US 2004219564 A1 20041104
US 6858742 B2 20050222
AI US 2003-689586 A1 20031022 (10)
RLI Division of Ser. No. US 2003-428137, filed on 2 May 2003, PENDING
DT Utility
FS APPLICATION
LREP BRUCE H. TROXELL, SUITE 1404, 5205 LEESBURGH PIKE, FALLS CHURCH, VA, 22041
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 3 Drawing Page(s)
LN.CNT 481
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to ***DNA*** labeling reagents comprising a furocoumarin derivative and a detectable group with or without bound via a binding enhancer, and acridinium-9-carboxamide derivatives for use as chemiluminescent labels. The present invention also relates to a process of preparing ***DNA*** labeling compound.

=> e huang chang/au
E1 2 HUANG CHANDLER M H/AU
E2 1 HUANG CHANDLER MARY H/AU
E3 19 --> HUANG CHANG/AU
E4 1 HUANG CHANG AN/AU
E5 1 HUANG CHANG BAO/AU
E6 1 HUANG CHANG BO/AU
E7 44 HUANG CHANG CANG/AU
E8 5 HUANG CHANG CHENG/AU
E9 8 HUANG CHANG CHI/AU
E10 1 HUANG CHANG CHING/AU
E11 12 HUANG CHANG CHIUN/AU
E12 1 HUANG CHANG CHUN/AU
=> s e3-e12 and (dna or nucleic)
L3 2 ("HUANG CHANG"/AU OR "HUANG CHANG AN"/AU OR "HUANG CHANG BAO"/AU

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               OR "HUANG CHANG BO"/AU OR "HUANG CHANG CANG"/AU OR "HUANG CHANG
               CHENG"/AU OR "HUANG CHANG CHI"/AU OR "HUANG CHANG CHING"/AU OR
              "HUANG CHANG CHIUN"/AU OR "HUANG CHANG CHUN"/AU) AND (DNA OR
              NUCLEIC)
=> dup rem l3
PROCESSING COMPLETED FOR L3
L4            2 DUP REM L3 (0 DUPLICATES REMOVED)
=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 2 ANSWERS - CONTINUE? Y/(N):y

L4   ANSWER 1 OF 2  USPATFULL on STN
AN     2003:10683  USPATFULL
TI     Erythritol-producing moniliella strains
IN     Lin, Shie-Jea, Hsinchu, TAIWAN, PROVINCE OF CHINA
       Wen, Chiou-Yen, Hsinchu, TAIWAN, PROVINCE OF CHINA
           ***Huang, Chang-Cheng***  , Keelung, TAIWAN, PROVINCE OF CHINA
       Chu, Wen-Shen, Hsinchu, TAIWAN, PROVINCE OF CHINA
PI     US 2003008378      A1   20030109
AI     US 2002-200730     A1   20020722 (10)
RLI    Division of Ser. No. US 2001-759778, filed on 12 Jan 2001, GRANTED, Pat.
       No. US 6455301
DT     Utility
FS     APPLICATION
LREP   Y. ROCKY TSAO, Fish & Richardson P.C., 225 Franklin Street, Boston, MA,
       02110-2804
CLMN   Number of Claims: 18
ECL    Exemplary Claim: 1
DRWN   No Drawings
LN.CNT 465
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     An isolated strain of the Moniliella species that converts glucose to
       erythritol with a conversion rate of at least about 45% is disclosed, as
       is a method of producing erythritol from such a strain.

L4   ANSWER 2 OF 2  USPATFULL on STN
AN     2002:243127  USPATFULL
TI     Erythritol - producing moniliella strains
IN     Lin, Shie-Jea, Hsinchu, TAIWAN, PROVINCE OF CHINA
       Wen, Chiou-Yen, Hsinchu, TAIWAN, PROVINCE OF CHINA
           ***Huang, Chang-Cheng***  , Keelung, TAIWAN, PROVINCE OF CHINA
       Chu, Wen-Shen, Hsinchu, TAIWAN, PROVINCE OF CHINA
PI     US 2002132313      A1   20020919
       US 6455301         B2   20020924
AI     US 2001-759778     A1   20010112 (9)
DT     Utility
FS     APPLICATION
LREP   Y. ROCKY TSAO, FISH & RICHARDSON P.C., 225 Franklin Street, Boston, MA,
       02110-2804
CLMN   Number of Claims: 18
ECL    Exemplary Claim: 1
DRWN   No Drawings
LN.CNT 465
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     An isolated strain of the Moniliella species that converts glucose to
       erythritol with a conversion rate of at least about 45% is disclosed, as
       is a method of producing erythritol from such a strain.
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* * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *
=> file caba caplus embase japio lifesci medline scisearch uspatfull
=> s (magnetic bead?) and (probe?)
L1        7227 (MAGNETIC BEAD?) AND (PROBE?)
=> dup rem l1
L2         6857 DUP REM L1 (370 DUPLICATES REMOVED)
=> s l2 and mycobact?
L3        1232 L2 AND MYCOBACT?
=> s l3 and hybridiz?
L4        1163 L3 AND HYBRIDIZ?
=> s l4 and (avidin or streptavidin)
L5        1048 L4 AND (AVIDIN OR STREPTAVIDIN)
=> s l5 and (method or assay)
L6        1048 L5 AND (METHOD OR ASSAY)

=> s l6 and (probe?(2w)magnetic bead?)
L7          15 L6 AND (PROBE?(2W) MAGNETIC BEAD?)


=> d bib 1-
YOU HAVE REQUESTED DATA FROM 15 ANSWERS - CONTINUE? Y/(N):y


L7   ANSWER 1 OF 15  USPATFULL on STN
AN     2005:10930  USPATFULL
TI     Nucleic acid detection and quantification using terminal transferase
       based assays
IN     Hassibi, Arjang, Palo Alto, CA, UNITED STATES
       Ghazvini, Siavash, Menlo Park, CA, UNITED STATES
PI     US 2005009064      A1   20050113
AI     US 2004-844674     A1   20040513 (10)
PRAI   US 2003-470347P     20030513 (60)
DT     Utility
FS     APPLICATION
LREP   BLAKELY SOKOLOFF TAYLOR & ZAFMAN, 12400 WILSHIRE BOULEVARD, SEVENTH
       FLOOR, LOS ANGELES, CA, 90025-1030
CLMN   Number of Claims: 35
ECL    Exemplary Claim: 1
DRWN   3 Drawing Page(s)
LN.CNT 1038
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7   ANSWER 2 OF 15  USPATFULL on STN
AN     2004:254319  USPATFULL
TI     Methods and apparatus for pathogen detection, identification and/or
       quantification
IN     Hassibi, Arjang, Palo Alto, CA, UNITED STATES
       Hassibi, Babak, San Marino, CA, UNITED STATES
       Ghazvini, Siavash, Menlo Park, CA, UNITED STATES
PI     US 2004197845      A1   20041007
AI     US 2003-627332     A1   20030724 (10)
PRAI   US 2002-407412P     20020830 (60)
       US 2002-422439P     20021029 (60)
       US 2002-435924P     20021220 (60)
       US 2002-435934P     20021220 (60)
       US 2003-440670P     20030115 (60)
       US 2003-451107P     20030227 (60)
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US 2003-470347P 20030513 (60)
DT Utility
FS APPLICATION
LREP Richard A. Nakashima, BLAKELY, SOKOLOFF, TAYLOR & ZAFMAN LLP, Seventh Floor, 12400 Wilshire Boulevard, Los Angeles, CA, 90025
CLMN Number of Claims: 48
ECL Exemplary Claim: 1
DRWN 34 Drawing Page(s)
LN.CNT 3755
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 3 OF 15 USPATFULL on STN
AN 2004:254267 USPATFULL
TI Methods and apparatus for biomolecule detection, identification, quantification and/or sequencing
IN Hassibi, Arjang, Palo Alto, CA, UNITED STATES
Hassibi, Babek, San Marino, CA, UNITED STATES
Ghazvini, Siavash, Menlo Park, CA, UNITED STATES
PI US 2004197793 A1 20041007
AI US 2003-627557 A1 20030724 (10)
PRAI US 2002-407412P 20020830 (60)
US 2002-422439P 20021029 (60)
US 2002-435924P 20021220 (60)
US 2002-435934P 20021220 (60)
US 2003-440670P 20030115 (60)
US 2003-451107P 20030227 (60)
US 2003-470347P 20030513 (60)
DT Utility
FS APPLICATION
LREP Blakely, Sokoloff, Taylor & Zafman, Seventh Floor, 12400 Wilshire Boulevard, Los Angeles, CA, 90025-1030
CLMN Number of Claims: 63
ECL Exemplary Claim: 1
DRWN 30 Drawing Page(s)
LN.CNT 3586
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 4 OF 15 USPATFULL on STN
AN 2004:178318 USPATFULL
TI Nucleic acid amplification methods
IN Zhang, David Y., Jamaica, NY, UNITED STATES
Zhang, Wandi, New York, NY, UNITED STATES
Yi, Jizu, Bayside, NY, UNITED STATES
PI US 2004137484 A1 20040715
AI US 2003-719480 A1 20031121 (10)
RLI Continuation-in-part of Ser. No. US 2001-978261, filed on 15 Oct 2001, PENDING Continuation-in-part of Ser. No. WO 2002-US32745, filed on 15 Oct 2002, PENDING
DT Utility
FS APPLICATION
LREP Steven B. Pokotilow, Stroock & Stroock & Lavan LLP, 180 Maiden Lane, New York, NY, 10038
CLMN Number of Claims: 55
ECL Exemplary Claim: 1
DRWN 28 Drawing Page(s)
LN.CNT 4225
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 5 OF 15 USPATFULL on STN
AN 2004:46156 USPATFULL
TI Nucleic acid amplification ***method*** ***hybridization*** signal amplification ***method*** (HSAM)
IN Zhang, David Y., Jamaica, NY, United States
Brandwein, Margaret, Jamaica, NY, United States
PA Mount Sinai School of Medicine, New York, NY, United States (U.S. corporation)
PI US 38442 E1 20040224
US 5876924 19990302 (Original)
AI US 2001-798641 20010302 (9)
US 1996-690495 19960731 (Original)
RLI Continuation-in-part of Ser. No. WO 1995-US7671, filed on 14 Jun 1995
Continuation-in-part of Ser. No. US 1996-596331, filed on 20 May 1996
Continuation-in-part of Ser. No. US 1994-263937, filed on 22 Jun 1994, now abandoned
DT Reissue
FS GRANTED
EXNAM Primary Examiner: Siew, Jeffrey; Assistant Examiner: Tung, Joyce
LREP Stroock & Stroock & Lavan LLP
CLMN Number of Claims: 17
ECL Exemplary Claim: 1,16,17
DRWN 21 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 3157
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 6 OF 15 USPATFULL on STN
AN 2003:271001 USPATFULL
TI Nucleic acid amplification ***method*** : ramification-extension amplification ***method*** (RAM)
IN Zhang, David Y., Jamaica, NY, UNITED STATES
Brandwein, Margaret, Jamaica Estates, NY, UNITED STATES
Hsuih, Terence C.H., Long Island City, NY, UNITED STATES
PI US 2003190604 A1 20031009
US 6855523 B2 20050215
AI US 2002-309438 A1 20021204 (10)
RLI Continuation of Ser. No. US 1999-299217, filed on 23 Apr 1999, GRANTED, Pat. No. US 6569647 Continuation of Ser. No. US 1996-690494, filed on 31 Jul 1996, GRANTED, Pat. No. US 5942391 Continuation-in-part of Ser. No. WO 1995-US7671, filed on 14 Jun 1995, PENDING Continuation-in-part of Ser. No. US 1994-263937, filed on 22 Jun 1994, ABANDONED
DT Utility
FS APPLICATION
LREP Steven B. Pokotilow, Stroock & Stroock & Lavan LLP, 180 Maiden Lane, New York, NY, 10038
CLMN Number of Claims: 46
ECL Exemplary Claim: 1
DRWN 13 Drawing Page(s)
LN.CNT 3034
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 7 OF 15 USPATFULL on STN
AN 2003:250920 USPATFULL
TI Nucleic acid amplification methods
IN Zhang, David Y., Jamaica, NY, UNITED STATES
PI US 2003175706 A1 20030918

AI US 2001-978261 A1 20011015 (9)
DT Utility
FS APPLICATION
LREP Steven B. Pokotilow, Esq., Stroock & Stroock & Lavan LLP, 180 Maiden Lane, New York, NY, 10038
CLMN Number of Claims: 39
ECL Exemplary Claim: 1
DRWN 24 Drawing Page(s)
LN.CNT 3394
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 8 OF 15 USPATFULL on STN
AN 2003:142941 USPATFULL
TI Nucleic acid amplification ***method*** : ramification-extension amplification ***method*** (RAM)
IN Zhang, David Y., Jamaica, NY, United States
Brandwein, Margaret, Jamaica Estates, NY, United States
Hsuih, Terence C. H., Long Island City, NY, United States
PA Mount Sinai School of Medicine of New York University, New York, NY, United States (U.S. corporation)
PI US 6569647 B1 20030527
AI US 1999-299217 19990423 (9)
RLI Continuation of Ser. No. US 1996-690494, filed on 31 Jul 1996, now patented, Pat. No. US 5942391, issued on 24 Aug 1999
Continuation-in-part of Ser. No. US 596331, now abandoned
Continuation-in-part of Ser. No. US 1994-263937, filed on 22 Jun 1994, now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: Whisenant, Ethan C.; Assistant Examiner: Lu, Frank
LREP Stroock & Stroock & Lavan LLP
CLMN Number of Claims: 33
ECL Exemplary Claim: 1
DRWN 21 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 3152
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 9 OF 15 USPATFULL on STN
AN 2002:322434 USPATFULL
TI Nucleic acid amplification methods
IN Zhang, David Y., Jamaica, NY, UNITED STATES
PI US 2002182598 A1 20021205
US 6593086 B2 20030715
AI US 2000-728265 A1 20001201 (9)
RLI Continuation-in-part of Ser. No. US 1999-299217, filed on 23 Apr 1999, PENDING Continuation of Ser. No. US 1996-690494, filed on 31 Jul 1996, PATENTED
DT Utility
FS APPLICATION
LREP BAKER BOTIS L.L.P., 44TH FLOOR, 30 ROCKEFELLER PLAZA, NEW YORK, NY, 10112-4498
CLMN Number of Claims: 30
ECL Exemplary Claim: 1
DRWN 19 Drawing Page(s)
LN.CNT 3841
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 10 OF 15 USPATFULL on STN
AN 2002:235380 USPATFULL
TI Two-step ***hybridization*** and capture of a polynucleotide
IN Weisburg, William G., San Diego, CA, UNITED STATES
Shaw, Jay H., San Diego, CA, UNITED STATES
Becker, Michael M., San Diego, CA, UNITED STATES
Majlessi, Mehrdad R., Escondido, CA, UNITED STATES
Brentano, Steven T., Santee, CA, UNITED STATES
Nunomura, Kiyotada, Tokyo, JAPAN
PI US 2002127569 A1 20020912
US 6534273 B2 20030318
AI US 2001-956412 A1 20010918 (9)
RLI Continuation-in-part of Ser. No. US 2001-910635, filed on 20 Jul 2001, PENDING Division of Ser. No. US 2000-574561, filed on 19 May 2000, GRANTED, Pat. No. US 6280952 Division of Ser. No. US 1998-70998, filed on 1 May 1998, GRANTED, Pat. No. US 6110678
PRAI US 1997-45430P 19970502 (60)
DT Utility
FS APPLICATION
LREP GEN PROBE INCORPORATED, 10210 GENETIC CENTER DRIVE, SAN DIEGO, CA, 92121
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 7 Drawing Page(s)
LN.CNT 2334
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 11 OF 15 USPATFULL on STN
AN 2002:48268 USPATFULL
TI Two-step ***hybridization*** and capture of a polynucleotide
IN Weisburg, William G., San Diego, CA, UNITED STATES
Shaw, Jay H., San Diego, CA, UNITED STATES
Becker, Michael M., San Diego, CA, UNITED STATES
Majlessi, Mehrdad, San Diego, CA, UNITED STATES
PI US 2002028459 A1 20020307
AI US 2001-910635 A1 20010720 (9)
RLI Division of Ser. No. US 2000-574561, filed on 19 May 2000, GRANTED, Pat. No. US 6280952 Division of Ser. No. US 1998-70998, filed on 1 May 1998, GRANTED, Pat. No. US 6110678
PRAI US 1997-45430P 19970502 (60)
DT Utility
FS APPLICATION
LREP Christine A. Gritzmacher, GEN-PROBE INCORPORATED, Patent Department, 10210 Genetic Center Drive, San Diego, CA, 92121
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 4 Drawing Page(s)
LN.CNT 1772
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 12 OF 15 USPATFULL on STN
AN 2001:142094 USPATFULL
TI Two-step ***hybridization*** and capture of a polynucleotide
IN Weisburg, William G., San Diego, CA, United States
Shaw, Jay H., San Diego, CA, United States
Becker, Michael M., San Diego, CA, United States
Majlessi, Mehrdad, San Diego, CA, United States
PA Gen-Probe Incorporated, San Diego, CA, United States (U.S. corporation)

PI US 6280952 B1 20010828
AI US 2000-574561 20000519 (9)
RLI Division of Ser. No. US 1998-70998, filed on 1 May 1998, now patented, Pat. No. US 6110678
DT Utility
FS GRANTED
EXNAM Primary Examiner: Whisenaut, Ethan
LREP Gritzmacher, Christine, Fisher, Carlos
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1901
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 13 OF 15 USPATFULL on STN
AN 2000:113706 USPATFULL
TI Two-step ***hybridization*** and capture of a polynucleotide
IN Weisburg, William G., San Diego, CA, United States
Shaw, Jay H., San Diego, CA, United States
Becker, Michael M., San Diego, CA, United States
Majlessi, Mehrdad, San Diego, CA, United States
PA Gen-Probe Incorporated, San Diego, CA, United States (U.S. corporation)
PI US 6110678 20000829
AI US 1998-70998 19980501 (9)
PRAI US 1997-45430P 19970502 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Whisenant, Ethan
LREP Gritzmacher, Christine A., Fisher, Carlos A.
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 4 Drawing Page(s)
LN.CNT 1839
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 14 OF 15 USPATFULL on STN
AN 1999:99539 USPATFULL
TI Nucleic acid amplification ***method*** : ramification-extension amplification ***method*** (RAM)
IN Zhang, David Y., Jamaica, NY, United States
Brandwein, Margaret, Jamaica Estates, NY, United States
Hsuih, Terence C. H., New York, NY, United States
PA Mount Sinai School of Medicine, New York, NY, United States (U.S. corporation)
PI US 5942391 19990824
AI US 1996-690494 19960731 (8)
RLI Continuation-in-part of Ser. No. WO 1995-US7671, filed on 14 Jun 1995 which is a continuation-in-part of Ser. No. US 1994-263937, filed on 22 Jun 1994, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Whisenant, Ethan
LREP Baker & Botts, LLP
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN 20 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 3188

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 15 OF 15 USPATFULL on STN
AN 1999:27388 USPATFULL
TI Nucleic acid amplification ***method*** ***hybridization*** signal amplification ***method*** (HSAM)
IN Zhang, David Y., Jamaica, NY, United States
Brandwein, Margaret, Jamaica Estates, NY, United States
PA Mount Sinai School of Medicine, New York, NY, United States (U.S. corporation)
PI US 5876924 19990302
AI US 1996-690495 19960731 (8)
RLI Continuation-in-part of Ser. No. US 1996-596331, filed on 20 May 1996 which is a continuation-in-part of Ser. No. US 1994-263937, filed on 22 Jun 1994, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Tung, Joyce
LREP Baker & Botts, LLP
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 21 Drawing Figure(s); 13 Drawing Page(s)
LN.CNT 2981
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> file uspatfull
=> s (magnetic bead?)/clm
141775 MAGNETIC/CLM
31497 BEAD?/CLM
L8 459 (MAGNETIC BEAD?)/CLM
((MAGNETIC(W)BEAD?)/CLM)
=> s l8 and mycobact?/clm
1645 MYCOBACT?/CLM
L9 5 L8 AND MYCOBACT?/CLM
=> d bib ab 1-
YOU HAVE REQUESTED DATA FROM 5 ANSWERS - CONTINUE? Y/(N):y

L9 ANSWER 1 OF 5 USPATFULL on STN
AN 2004:239649 USPATFULL
TI Method of detecting pathogenic microorganism
IN Shimada, Masamitsu, Otsu-shi, JAPAN
Hino, Fumitsugu, Kusatsu-shi, JAPAN
Kato, Ikunoshin, Uji-shi, JAPAN
PI US 2004185455 A1 20040923
AI US 2003-451882 A1 20030626 (10)
WO 2001-JP11422 20011226
PRAI JP 2000-396222 20001226
JP 2000-396321 20001226
JP 2001-199552 20010629
JP 2001-278920 20010913
DT Utility
FS APPLICATION
LREP BROWDY AND NEIMARK, P.L.L.C., 624 NINTH STREET, NW, SUITE 300, WASHINGTON, DC, 20001-5303
CLMN Number of Claims: 77
ECL Exemplary Claim: 1

DRWN 1 Drawing Page(s)
LN.CNT 3180
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Oligonucleotide probes and primers useful in detecting pathogenic microorganisms; a method of detecting a pathogenic microorganism by using the same; and kits for this method.

L9 ANSWER 2 OF 5 USPATFULL on STN
AN 2004:209355 USPATFULL
TI Sample processing
IN Chen, Shuqi, Brookline, MA, UNITED STATES
Lemieux, Bertrand, Brighton, MA, UNITED STATES
Wang, Zihua, Newton, MA, UNITED STATES
Kopczynski, Kevin R., Cambridge, MA, UNITED STATES
Chen, Lingjum, Brookline, MA, UNITED STATES
PI US 2004161788 A1 20040819
AI US 2004-773775 A1 20040205 (10)
PRAI US 2003-445304P 20030205 (60)
DT Utility
FS APPLICATION
LREP FOLEY HOAG, LLP, PATENT GROUP, WORLD TRADE CENTER WEST, 155 SEAPORT BLVD, BOSTON, MA, 02110
CLMN Number of Claims: 75
ECL Exemplary Claim: 1
DRWN 7 Drawing Page(s)
LN.CNT 2030
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A sample processing tubule may include a first segment, a second segment, and a third segment. Each segment may be defined by the tubule, may be fluidly isolated, at least in part by a breakable seal, may be so expandable as to receive a volume of fluid expelled from another segment, and may be so compressible as to contain substantially no fluid when so compressed. Each segment may contain at least one reagent.

L9 ANSWER 3 OF 5 USPATFULL on STN
AN 2001:67386 USPATFULL
TI Chip-based species identification and phenotypic characterization of microorganisms
IN Gingeras, Thomas R., Encinitas, CA, United States
Mack, David, Menlo Park, CA, United States
Chee, Mark S., Palo Alto, CA, United States
Berno, Anthony J., San Jose, CA, United States
Stryer, Lubert, Stanford, CA, United States
Ghandour, Ghassan, Atherton, CA, United States
Wang, Ching, San Jose, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6228575 B1 20010508
AI US 1997-797812 19970207 (8)
RLI Continuation-in-part of Ser. No. US 1996-629031, filed on 8 Apr 1996, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Townsend and Townsend and Crew LLP
CLMN Number of Claims: 97
ECL Exemplary Claim: 1
DRWN 44 Drawing Figure(s); 34 Drawing Page(s)

LN.CNT 3109
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides oligonucleotide based arrays and methods for speciating and phenotyping organisms, for example, using oligonucleotide sequences based on the Mycobacterium tuberculosis rpoB gene. The groups or species to which an organism belongs may be determined by comparing hybridization patterns of target nucleic acid from the organism to hybridization patterns in a database.

L9 ANSWER 4 OF 5 USPATFULL on STN
AN 2000:113712 USPATFULL
TI Mismatch detection techniques
IN Kemper, Borries, Koln, Germany, Federal Republic of
Birkenkamp-Demtroder, Karin, Solingen, Germany, Federal Republic of
Golz, Stefan, Essen, Germany, Federal Republic of
PA Variagenics, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6110684 20000829
AI US 1999-243558 19990202 (9)
PRAI US 1998-73716P 19980204 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Myers, Carla J.; Assistant Examiner: Johannsen, Diana
LREP Clark & Elbing LLP
CLMN Number of Claims: 50
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 1031
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed herein is a method for detecting a mismatch in a duplex nucleic acid, involving: a) contacting the duplex nucleic acid with a reactive agent under conditions which permit the agent to bind but not cleave a mismatch in said duplex nucleic acid; b) detecting binding of the agent to the duplex nucleic acid as an indication of the presence of a mismatch in the duplex nucleic acid; c) contacting the duplex nucleic acid with the reactive agent under conditions which permit the agent to cleave a mismatch in the duplex nucleic acid; and d) detecting a cleavage product as an indication of the presence of a mismatch in the duplex nucleic acid.

L9 ANSWER 5 OF 5 USPATFULL on STN
AN 1998:111760 USPATFULL
TI Mycobacterial nucleic acid hybridization probes and methods of use
IN Guesdon, Jean-Luc, Paris, France
Thierry, Dominique, Boulogne, France
Ullman, Agnes, Paris, France
Gicquel, Brigitte, Paris, France
Brisson-Noel, Anne, Paris, Francë
PA Institut Pasteur, Paris, France (non-U.S. corporation)
PI US 5807672 19980915
AI US 1995-487651 19950607 (8)
RLI Continuation of Ser. No. US 1992-829016, filed on 14 Apr 1992, now patented, Pat. No. US 5597911
PRAI FR 1989-11665 19890906
FR 1990-2676 19900302
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Tung, Joyce

LREP Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 9 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1173
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fragments of nucleic acids derived from an appropriate mycobacteria genome, particularly Mycobacterium tuberculosis, their applications in the diagnosis of mycobacteria infections, as well as plasmides containing said fragments. The nucleotidic sequence is comprised of a nucleotidic sequence repeated in the genome of a mycobacterium and specific of the bacillus of tuberculosis and is characterized by a strong hybridation with M. tuberculosis.

=> s l9 and hybridiz?/clm
19652 HYBRIDIZ?/CLM
L10 3 L9 AND HYBRIDIZ?/CLM
=> d bib ab kwic
L10 ANSWER 1 OF 3 USPATFULL on STN
AN 2004:239649 USPATFULL
TI Method of detecting pathogenic microorganism
IN Shimada, Masamitsu, Otsu-shi, JAPAN
Hino, Fumitsugu, Kusatsu-shi, JAPAN
Kato, Ikunoshin, Uji-shi, JAPAN
PI US 2004185455 A1 20040923
AI US 2003-451882 A1 20030626 (10)
WO 2001-JP11422 20011226
PRAI JP 2000-396222 20001226
JP 2000-396321 20001226
JP 2001-199552 20010629
JP 2001-278920 20010913
DT Utility
FS APPLICATION
LREP BROWDY AND NEIMARK, P.L.L.C., 624 NINTH STREET, NW, SUITE 300, WASHINGTON, DC, 20001-5303
CLMN Number of Claims: 77
ECL Exemplary Claim: 1
DRWN 1 Drawing Page(s)
LN.CNT 3180
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Oligonucleotide probes and primers useful in detecting pathogenic microorganisms; a method of detecting a pathogenic microorganism by using the same; and kits for this method.
CLM What is claimed is:
. . . probe containing the nucleotide sequence of SEQ ID NO:39 or a part thereof, which can be used to detect a ***Mycobacterium*** tuberculosis complex ***Mycobacterium*** tuberculosis, ***Mycobacterium*** bovis BCG, ***Mycobacterium*** africanum, ***Mycobacterium*** microti and/or ***Mycobacterium*** canetti.

2. A probe consisting of the nucleotide sequence of SEQ ID NO:11, which can be used to detect a ***Mycobacterium*** tuberculosis complex ***Mycobacterium*** tuberculosis, ***Mycobacterium*** bovis BCG, ***Mycobacterium*** africanum, ***Mycobacterium*** microti and/or ***Mycobacterium*** canetti.

8. A probe that can ***hybridize*** to a target nucleic acid from a pathogenic microorganism at alkaline pH.

9. The probe according to claim 8, which can ***hybridize*** to a target nucleic acid from a pathogenic microorganism at alkaline pH of 8 to 14.

10. The probe according to claim 8 or 9, wherein the pathogenic microorganism is a ***Mycobacterium*** tuberculosis complex, a gonococcus, a chlamydia or HCV.

. . . the target nucleic acid from a pathogenic microorganism is selected from a nucleotide sequence of IS 6110 gene from a ***Mycobacterium*** tuberculosis complex, a nucleotide sequence of cppB gene from a gonococcus, a nucleotide sequence of pLGV440 from a chlamydia or. . . . . or a part thereof, wherein the nucleotide sequence of SEQ ID NO:39 is present in IS 6110 gene from a ***Mycobacterium*** tuberculosis complex.

. . . 21, 34 or 35, and which is fluorescence-labeled such that the fluorescence intensity is not repressed if the probe is ***hybridized*** to the target nucleic acid, and the fluorescence intensity is repressed if the probe is not ***hybridized*** to the target nucleic acid.

27. A method for detecting a pathogenic microorganism, the method comprising conducting ***hybridization*** of the probe defined by any one of claims 1 to 26 to a target nucleic acid from a pathogenic. . .

28. The method according to claim 27, wherein the ***hybridization*** to a target nucleic acid from a pathogenic microorganism is conducted at alkaline pH.

29. The method according to 27 or 28, wherein the pathogenic microorganism is a ***Mycobacterium*** tuberculosis complex, a gonococcus, a chlamydia or HCV.

. . . method according to claim 29, wherein the target nucleic acid from a pathogenic microorganism is IS 6110 gene from a ***Mycobacterium*** tuberculosis complex or a fragment thereof.

31. The method according to claim 30, wherein ***hybridization*** of the probe defined by any one of claims 1, 2, 9 to 11, 12, 13 and 20 to 26 to amplified IS 6110 gene from a ***Mycobacterium*** tuberculosis complex and/or a fragment thereof is conducted.

32. The method according to claim 31, wherein IS 6110 gene from a ***Mycobacterium*** tuberculosis complex and/or a fragment thereof is amplified using a primer having the nucleotide sequence of SEQ ID NO:36 or. . .

34. The method according to claim 33, wherein ***hybridization*** of the probe defined by any one of claims 3, 4, 9 to 11, 14, 15 and 20 to 26. . .

37. The method according to claim 36, wherein ***hybridization*** of the probe defined by any one of claims 5, 6, 9 to 11, 16, 17 and 20 to 26. . .

40. The method according to claim 39, wherein ***hybridization*** of

the probe defined by any one of claims 7, 8, 9 to 11, 18, 19 and 20 to 26. . .

42. A method for detecting a pathogenic microorganism, the method comprising detecting a nucleic acid from a ***Mycobacterium*** tuberculosis complex, a gonococcus, a chlamydia or HCV using the method defined by any one of claims 27 to 41.

. . .

54. A primer for amplifying IS 6110 gene from a ***Mycobacterium*** tuberculosis complex and/or a fragment thereof, which has the nucleotide sequence of SEQ ID NO:36 or 37 or a sequence. . .

. . . NOS:13 to 16, 23 to 26 and 28 to 31; (v) a primer for amplifying IS 6110 gene from a ***Mycobacterium*** tuberculosis complex and/or a fragment thereof, which has the nucleotide sequence of SEQ ID NO:36 or 37 or a sequence. . .

70. The kit according to claim 68 or 69, wherein the pathogenic microorganism is a ***Mycobacterium*** tuberculosis complex, a gonococcus, a chlamydia or HCV.

. . . according to claim 75, wherein the support is selected from the group consisting of a microtiter plate, a bead, a ***magnetic*** ***bead*** , a membrane and glass.

77. A method for detecting a ***Mycobacterium*** tuberculosis complex, the method comprising treating a test sample containing a ***Mycobacterium*** tuberculosis complex with muramidase to extract a nucleic acid.

L10 ANSWER 2 OF 3 USPATFULL on STN
AN 2001:67386 USPATFULL
TI Chip-based species identification and phenotypic characterization of microorganisms
IN Gingeras, Thomas R., Encinitas, CA, United States
Mack, David, Menlo Park, CA, United States
Chee, Mark S., Palo Alto, CA, United States
Berno, Anthony J., San Jose, CA, United States
Stryer, Lubert, Stanford, CA, United States
Ghandour, Ghassan, Atherton, CA, United States
Wang, Ching, San Jose, CA, United States
PA Affymetrix, Inc., Santa Clara, CA, United States (U.S. corporation)
PI US 6228575 B1 20010508
AI US 1997-797812 19970207 (8)
RLI Continuation-in-part of Ser. No. US 1996-629031, filed on 8 Apr 1996, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Townsend and Townsend and Crew LLP
CLMN Number of Claims: 97
ECL Exemplary Claim: 1
DRWN 44 Drawing Figure(s); 34 Drawing Page(s)
LN.CNT 3109
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides oligonucleotide based arrays and methods for speciating and phenotyping organisms, for example, using oligonucleotide

sequences based on the Mycobacterium tuberculosis rpoB gene. The groups or species to which an organism belongs may be determined by comparing hybridization patterns of target nucleic acid from the organism to hybridization patterns in a database.

CLM What is claimed is:

. . . substrate, said array comprising probes complementary to reference DNA or RNA sequences from a second organism; (b) obtaining a first ***hybridization*** pattern by ***hybridizing*** a target nucleic acid sequence from the first organism to the array; and (c) comparing the first ***hybridization*** pattern of the first organism to a second ***hybridization*** pattern obtained by ***hybridizing*** a target nucleic acid sequence from the second organism to the array, wherein differences between the first and second ***hybridization*** patterns are indicative that the first organism is assigned to a particular group or species.

2. The method of claim 1, wherein the second organism is ***Mycobacterium*** tuberculosis.

4. The method of claim 3, wherein the differences in ***hybridization*** patterns are indicative of resistance to an antibiotic drug.

10. The method of claim 1, wherein the ***hybridizing*** is performed in a fluid volume of 250 .mu.l or less.

. . . presence of a nucleic acid polymorphism in a patient sample, comprising the steps of: (a) determining the difference between the ***hybridization*** intensities of a nucleic acid sequence from the patient sample and a corresponding nucleic acid sequence from a wild type sample to an array of reference nucleic acid probes; (b) deriving ratios of the difference in (a) to the ***hybridization*** intensity of the wild type sample for each base position corresponding to each reference nucleic acid probe; and (c) identifying. . .

. . . of a plurality of known nucleic acid sequences, the plurality of known nucleic acid sequences being from known organisms; inputting ***hybridization*** patterns for the plurality of known nucleic acid sequences, each ***hybridization*** pattern indicating ***hybridization*** of subsequences of the known nucleic acid sequence to subsequences of a reference nucleic acid sequence; inputting a ***hybridization*** pattern for a sample nucleic acid sequence from the organism indicating ***hybridization*** of subsequences of the sample nucleic acid sequence to subsequences of the reference nucleic acid sequence; comparing the ***hybridization*** pattern for the sample nucleic acid sequence to the ***hybridization*** patterns for the plurality of known nucleic acid sequences; and assigning a particular group to which the organism belongs according to the group of at least one of the known nucleic acid sequences that has a ***hybridization*** pattern that most closely matches the ***hybridization*** pattern of the sample nucleic acid sequence at specific locations.

21. The method of claim 18, further comprising the step of normalizing ***hybridization*** intensities of the ***hybridization*** patterns of the sample and known nucleic acid sequences using linear regression.

23. The method of claim 18, further comprising the step of generating a database of the ***hybridization*** patterns for the plurality of known nucleic acid sequences.

24. The method of claim 18, wherein the reference nucleic acid sequence is from ***Mycobacterium*** tuberculosis.

28. The method of claim 18, wherein the group is a species of ***Mycobacterium*** .

31. A computer program product that assigns an organism to a group, comprising: computer code that receives as input groups. . . nucleic acid sequences, the plurality of known nucleic acid sequences being from known organisms; computer code that receives as input ***hybridization*** patterns for the plurality of known nucleic acid sequences, each ***hybridization*** pattern indicating ***hybridization*** of subsequences of the known nucleic acid sequence to subsequences of a reference nucleic acid sequence; computer code that receives as input a ***hybridization*** pattern for a sample nucleic acid sequence from the organism indicating ***hybridization*** of subsequences of the sample nucleic acid sequence to subsequences of the reference nucleic acid sequence; computer code that compares the ***hybridization*** pattern for the sample nucleic acid sequence to the ***hybridization*** patterns for the plurality of known nucleic acid sequences; computer code that assigns a particular group to which the organism belongs according to the groups of at least one of the known nucleic acid sequences that has a ***hybridization*** pattern that most closely matches the ***hybridization*** pattern of the sample nucleic acid sequence at specific locations; and a computer readable medium that stores the computer codes.

. . .

. . . A computerized method of assigning groups to which organisms belong utilizing a generic probe array, comprising the steps of: inputting ***hybridization*** intensities for a plurality of isolates, the ***hybridization*** intensities indicating ***hybridization*** affinity between the isolate and the generic probe array; selecting ***hybridization*** intensities that have the most variance across the plurality of isolates; and assigning each of the plurality of isolates to a group according to the selected ***hybridization*** intensities.

. . . 32, wherein the assigning step comprises the step of clustering the plurality of isolates into groups according to the selected ***hybridization*** intensities.

36. The method of claim 32, further comprising the step of standardizing the ***hybridization*** intensities among the plurality of isolates.

37. The method of claim 36, wherein the standardizing step comprises the step of adjusting the ***hybridization*** intensities of each isolate so that there is a common mean and variance across the plurality of isolates.

. . . product that assigns groups to which organisms belong utilizing a

generic probe array, comprising: computer code that receives as input ***hybridization*** intensities for a plurality of isolates, the ***hybridization*** intensities indicating ***hybridization*** affinity between the isolate and the generic probe array; computer code that selects ***hybridization*** intensities that have the most variance across the plurality of isolates; computer code that assigns a group to each of the plurality of isolates according to the selected ***hybridization*** intensities; and a computer readable medium that stores the computer codes.

42. A method of assigning a probability that at least a subset of a sample ***hybridization*** pattern is associated with one or more species, comprising: providing a first array of polynucleotides at known locations on a substrate; ***hybridizing*** a first nucleic acid to said first array to obtain a first ***hybridization*** pattern; providing a second array of polynucleotides at known locations on a substrate, wherein at least a subset of said polynucleotides of said second array comprises a subset of said polynucleotides of said first array; ***hybridizing*** a second nucleic acid to said second array to obtain a second ***hybridization*** pattern; comparing at least a portion of said first and second ***hybridization*** patterns and assigning a probability, based on said comparing, that the appearance of said portion in a sample ***hybridization*** pattern is associated with one or more species.

. . . of claim 42, further comprising repeating at least once said steps before said comparing step to obtain a plurality of ***hybridization*** patterns for use in said comparing step.

44. The method of claim 42, wherein a further ***hybridization*** pattern is obtained as a result of said comparing step.

45. The method of claim 44, wherein said further ***hybridization*** pattern is based upon similarities between said ***hybridization*** patterns compared in said comparing steps.

46. The method of claim 44, wherein said further ***hybridization*** pattern is based upon differences between said ***hybridization*** patterns compared in said comparing step.

47. The method of claim 44, wherein said further ***hybridization*** pattern is based upon similarities and differences between said ***hybridization*** patterns compared in said comparing step.

48. A ***hybridization*** pattern obtained by the method of claim 42.

49. The method of claim 42, wherein said assignment of said probability is based upon similarities between said ***hybridization*** patterns compared to said comparing step.

50. The method of claim 42, wherein said assignment of said probability is based upon differences between said ***hybridization*** patterns compared to said comparing step.

. . . 51. The method of claim 42, wherein said assignment of said probability is based upon similarities and differences between said

hybridization patterns compared to said comparing step.

. . . of claim 43, further comprising after said comparing step calling at least one base of at least one nucleic acid ***hybridized*** to said array in at least one of said repeated steps.

54. The method of claim 42, wherein said at least one of said ***hybridization*** patterns is a bar code.

55. The method of claim 42, wherein at least one of said ***hybridization*** patterns is intensity versus nucleotide position.

56. The method of claim 42, wherein at least one of said species is a species of ***Mycobacterium*** .

57. The method of claim 56, wherein said species of ***Mycobacterium*** is M. tuberculosis.

. . . the presence of a nucleic acid polymorphism in a patient sample, comprising: computer code that determines the difference between the ***hybridization*** intensities of a nucleic acid sequence from the patient sample and a corresponding nucleic acid sequence from a wild type sample to an array of reference nucleic acid probes; computer code that derives ratios of the difference to the ***hybridization*** intensity of the wild type sample for each base position corresponding to each reference nucleic acid probe; computer code that. . .

. . . substrate, said array comprising probes complementary to reference DNA or RNA sequences from a second organism; (b) obtaining a first ***hybridization*** pattern by ***hybridizing*** a target nucleic acid sequence from the first organism to the array; (c) comparing the first ***hybridization*** pattern of the first organism to a second ***hybridization*** pattern obtained by ***hybridizing*** a target nucleic acid sequence from the second organism to the array; (d) deriving one or more sets of differences between the first and second ***hybridization*** patterns; (e) comparing the set of differences to a data base comprising sets of differences correlated with speciation of organisms. . .

62. The method of claim 61, wherein the second organism is ***Mycobacterium*** tuberculosis.

70. The method of claim 61, wherein the ***hybridizing*** is performed in a fluid volume of 250 uL or less.

. . . nucleic acid sequence from the second organism is labeled, and the label is selected from the group consisting of biotin, ***magnetic*** ***beads*** , fluorescent dyes, radiolabels, enzymes, colorimetric labels and plastic beads.

. . . nucleic acid sequence from the second organism is labeled, and the label is selected from the group consisting of biotin, ***magnetic*** ***beads*** , fluorescent dyes, radiolabels, enzymes, colorimetric labels and plastic beads.

. . . disease is caused by a bacteria selected from the group consisting of Escherichia coli, Salmonella, Shigella, Klebsiella, Pseudomonas, Listeria monocytogenes, ***Mycobacterium*** tuberculosis,

Mycobacterium avium-intracellulare, Yersinia, Francisella, Pasteurella, Brucella, Clostridia, Bordetella pertussis, Bacteroides, Staphylococcus aureus, Streptococcus pneumonia, B-Hemolytic strep., Corynebacteria, Legionella, Mycoplasm, Ureaplasma, Chlamydia,. . . . . disease is caused by a bacteria selected from the group consisting of Escherichia coli, Salmonella, Shigella, Klebsiella, Pseudomonas, Listeria monocytogenes, ***Mycobacterium*** tuberculosis, ***Mycobacterium*** avium-intracellulare, Yersinia, Francisella, Pasteurella, Brucella, Clostridia, Bordetella pertussis, Bacteroides, Staphylococcus aureus, Streptococcus pneumonia, B-Hemolytic strep., Corynebacteria, Legionella, Mycoplasm, Ureaplasma, Chlamydia,. . . . . substrate, said array comprising probes complementary to reference DNA or RNA sequences from a second organism; (b) obtaining a first ***hybridization*** pattern by ***hybridizing*** a target nucleic acid sequence from the first organism to the array; and (c) comparing the first ***hybridization*** pattern of the first organism to a second ***hybridization*** pattern obtained by ***hybridizing*** a target nucleic acid sequence from the second organism to the array, wherein differences between the first and second ***hybridization*** patterns are indicative of phenotypic information assigned to the first organism.

87. The method of claim 2, wherein the reference DNA or RNA sequences are selected from the ***Mycobacterium*** tuberculosis genome.

88. The method of claim 1 wherein the differences in ***hybridization*** patterns are indicative of resistance to an antibiotic drug.

89. A computerized method of assigning an organism to a group, comprising the steps of: inputting ***hybridization*** patterns for a plurality of organisms, each of the organisms belonging to a known group, each ***hybridization*** pattern indicating ***hybridization*** of subsequences of the organism belonging to a known group to subsequences of a reference nucleic acid sequence; inputting a ***hybridization*** pattern for a sample nucleic acid sequence from an organism not assigned to a group indicating ***hybridization*** of subsequences of the sample nucleic acid sequence to subsequences of the reference nucleic acid sequence; comparing the ***hybridization*** pattern for the sample nucleic acid sequence to the ***hybridization*** patterns for the plurality of organisms, each of the organisms belonging to known group; and assigning a particular group to which the organism belongs according to the group of at least one of the organisms that has a ***hybridization*** pattern that most closely matches the ***hybridization*** pattern of the sample nucleic acid sequence at specific locations.

92. The method of claim 89, wherein the reference nucleic acid sequence is from ***Mycobacterium*** tuberculosis.

96. The method of claim 89, wherein the group is a species of ***Mycobacterium*** .

97. A computer program product that assigns an organism to a group, comprising: computer code that receives as input ***hybridization*** patterns for a plurality of organisms, each of the organisms belonging

to a known group, each ***hybridization*** pattern indicating ***hybridization*** of subsequences of the organism belonging to a known group to subsequences of a reference nucleic acid sequence; computer code that receives as input a ***hybridization*** pattern for a sample nucleic acid sequence from an organism not assigned to a group indicating ***hybridization*** of subsequences of the sample nucleic acid sequence to subsequences of the reference nucleic acid sequence; computer code that compares the ***hybridization*** pattern for the sample nucleic acid sequence to the ***hybridization*** patterns for the plurality of organisms, each organism belonging to a known group; computer code that assigns a particular group to which the organism belongs according to the group of at least one of the organisms that has a ***hybridization*** pattern that most closely matches the ***hybridization*** pattern of the sample nucleic acid sequence at specific locations; and a computer readable medium that stores the computer codes.

. . .

L10 ANSWER 3 OF 3 USPATFULL on STN
AN 1998:111760 USPATFULL
TI Mycobacterial nucleic acid hybridization probes and methods of use
IN Guesdon, Jean-Luc, Paris, France
Thierry, Dominique, Boulogne, France
Ullman, Agnes, Paris, France
Gicquel, Brigitte, Paris, France
Brisson-Noel, Anne, Paris, France
PA Institut Pasteur, Paris, France (non-U.S. corporation)
PI US 5807672 19980915
AI US 1995-487651 19950607 (8)
RLI Continuation of Ser. No. US 1992-829016, filed on 14 Apr 1992, now patented, Pat. No. US 5597911
PRAI FR 1989-11665 19890906
FR 1990-2676 19900302
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Tung, Joyce
LREP Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
CLMN Number of Claims: 21
ECL Exemplary Claim: 1
DRWN 9 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 1173
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Fragments of nucleic acids derived from an appropriate mycobacteria genome, particularly Mycobacterium tuberculosis, their applications in the diagnosis of mycobacteria infections, as well as plasmides containing said fragments. The nucleotidic sequence is comprised of a nucleotidic sequence repeated in the genome of a mycobacterium and specific of the bacillus of tuberculosis and is characterized by a strong hybridation with M. tuberculosis.
CLM What is claimed is:
. . . provided that said nucleotide sequence in which nucleotides have been deleted and said nucleotide sequence which contains additional nucleotides specifically ***hybridize*** to the DNA of SEQ ID NO:3.

6. The DNA of claim 4, wherein said solid support comprises ***magnetic*** ***beads*** .

7. A purified DNA, consisting of a nucleotide sequence of from 20 nucleotides to 1358 nucleotides in length, which ***hybridizes*** exclusively to the polynucleotide of SEQ ID NO:3 under the following conditions: prehybridizing the polynucleotide of SEQ ID NO:3 for 15 minutes at 65.degree. C.; ***hybridizing*** the purified DNA with the polynucleotide of SEQ ID NO:3 for 2 hours at 65.degree. C.; washing twice for 10. . .

. . . in SEQ ID NO:3, comprising (1) producing a recombinant cosmid library containing DNA inserts larger than 30 kb from a ***mycobacterium*** of said tuberculosis bacillus group; and (2) detecting a cosmid clone containing said repetitive sequence by ***hybridizing*** said cosmid clone to a labeled DNA of claim 1.

9. A method of detecting a tuberculosis bacillus group ***mycobacterium*** of ***Mycobacterium*** bovis BCG in a biological sample, comprising (1) contacting said biological sample with the DNA of claim 1 to obtain a ***hybridization*** product between said biological sample and said DNA; and (2) detecting said ***hybridization*** product.

12. A method of detecting a tuberculosis bacillus group ***mycobacterium*** or ***Mycobacterium*** bovis BCG in a biological sample containing DNA, comprising (1) specifically ***hybridizing*** the DNA of claim 1 with said DNA in said biological sample, to obtain a ***hybridized*** product; (2) elongating said ***hybridized*** product to produce an elongation product having two strands; (3) separating said strands; (4) repeating steps (1), (2) and (3). . .

14. A kit ready for use for detecting a tuberculosis bacillus group ***mycobacterium*** or ***Mycobacterium*** bovis BCG in a biological sample, comprising: (a) the DNA of claim 1; (b) reagents for extracting said DNA in. . . said biological sample from said biological sample; (c) reagents for amplifying DNA; (d) at least one nucleotide probe which specifically ***hybridizes*** to the DNA of formula SEQ ID NO:3; (e) an internal standard, comprising DNA containing a gene for resistance to. . . provided that said nucleotide sequence in which nucleotides have been deleted and said nucleotide sequence which contains additional nucleotides specifically ***hybridize*** to the DNA of formula SEQ ID NO:3; and (f) a probe which specifically ***hybridizes*** to said DNA of said internal standard.

16. The kit of claim 14, further comprising means for making ***hybridization*** visible.

19. A method of detecting a tuberculosis bacillus group ***mycobacterium*** or ***Mycobacterium*** bovis BCG in a biological sample, comprising (1) contacting said biological sample with DNA selected from the group consisting of:. . . SEQ ID NO:5 an d SEQ ID NO:10; and (f) SEQ ID NO:4 and SEQ ID NO:6, to obtain a ***hybridization*** product between said biological sample and said DNA providing a DNA fragment to be amplified; (2) amplifying said DNA fragment;. . .

21. Purified DNA primers for the amplification of ***mycobacterial*** DNA, selected from the group consisting of: (a) SEQ ID NO:5 and SEQ ID NO:10; and (b) SEQ ID NO:4. . .